



Revised March 29, 2004- 39754-0611 US.txt

SEQUENCE LISTING

<110> WALKER, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> 39754-0611-1CP1CP

<140> US 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> US 08/594,809

<151> 1996-01-31

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (622)...(624)

<223> This is the codon for the substituted amino acids of the mutated sequence.

<400> 1

aacatgaaca tcaaaggatc gccatggaaa gggccctcc tgctgctgct ggtgtcaaac 60  
ctgctgctgt gccagagcgt ggccccccttg cccatctgtc ccggcggggc tgcccgatgc 120  
caggtgaccc ttcgagacct gtttgaccgc gccgtcgtcc tgtcccacta catccataac 180  
ctctcctcag aaatgttcag cgaattcgat aaacggata cccatggccg ggggttcatt 240  
accaaggcca tcaacagctg ccacacttct tcccttgcca cccccaaga caaggagcaa 300  
gcccaacaga tgaatcaaaa agactttctg agcctgatag tcagcatatt gcgatcctgg 360  
aatgagcctc tgtatcatct ggtcacggaa gtacgtggta tgcaagaagc cccggaggct 420  
atcctatcca aagctgtaga gattgaggag caaaccacaa ggcttctaga gggcatggag 480  
ctgatagtca gccaggttca tcctgaaacc aaagaaaatg agatctaccc tgtctggtcg 540  
ggacttccat ccctgcagat ggctgatgaa gagtctcgcc tttctgctta ttataacctg 600  
ctccactgcc tacgcagggta tnnncataaaa atcgacaatt atctcaagct cctgaagtgc 660  
cgaatcatcc acaacaacaa ctgctaagcc cacatccatt tcatttattt ctgagaaggt 720  
ccttaatgtat ccgttccatt gcaagcttct tttagttgta tctctttga atccatgctt 780  
gggtgtaaca ggtctcctct taaaaaataa aaactgactc gtttagagaca tc 832

<210> 2

<211> 228

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 208

<223> site mutated amino acid residue where the normal codon coding for serine is modified preferably to encode for aspartate or glutamate, most preferably aspartate.

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<400> 2  
Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu  
1 5 10 15  
Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile  
20 25 30  
Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe  
35 40 45  
Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu  
50 55 60  
Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile  
65 70 75 80  
Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu  
85 90 95  
Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu  
100 105 110  
Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val  
115 120 125  
Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys  
130 135 140  
Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu  
145 150 155 160  
Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr  
165 170 175  
Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser  
180 185 190  
Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa  
195 200 205  
His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His  
210 215 220  
Asn Asn Asn Cys  
225

<210> 3

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<400> 3

gcagggatga ccacaagggtt gac

23

<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<220>

<221> variation

<222> 12

<223> This is a nucleic acid residue that can be replaced for nucleic acid substitutes.

<400> 4

cgcaaggat gnacacaagg ttga

24

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<220>

<221> variation

<222> 12

<223> This is a nucleic acid residue that can be replaced for nucleic acid substitutes.

<400> 5

acgcaggat gnkataaaat cg

22

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<400> 6

cgtggccccc atatgttgcc catctg

26